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Taxonomy and functional roles of biogas microbiota binned from multiple metagenomes of anaerobic digestion systems

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Anaerobic digestion, a biologically mediated process, is a worldwide spread technology for biogas production. This work represents the first comprehensive catalogue of microbial genomes populating mesophilic and thermophilic biogas reactors treating manure, agro-industrial organic residues. High throughput Illumina sequencing was performed on samples collected from 22 biogas reactors (laboratory and full scale) operating under different conditions. Using a binning strategy, 575 high quality microbial genome bins were extracted and abundance-weighted community composition was determined. Average nucleotide identity grouped the genomes in 373 different species. Phylogeny and taxonomy assignment at species/genus level was possible only for 12% of the community members demonstrating a high degree of novelty in this microbiome. Moreover, 21 highly abundant genomes were found to be present in all digesters and constitute the community core group. Interestingly, 42% of them were classified as belonging to the *Syntrophomonadaceae* family. A correlation between the community composition resilience and the microbial functional specialization was also established. The core functional properties were found to cover all the steps of the anaerobic digestion process, from hydrolysis to methanogenesis. On contrary, 4 groups of genomes were identified only in specific bioreactors and therefore were found to be dependent on the operational parameters. Despite specific, some of these genomes are crucial for a properly functioning microbiome since they operate in peculiar conditions, determined by lipids and polysaccharides overload or in the presence of ammonia inhibition. Remarkably, by combining community composition and functional properties we provided a clear understanding of the anaerobic digestion process.